L Number	Hits	Search Text	DB	Time stamp
1	0	gtni or gtn adj I	USPAT	2001/12/18 13:33
2	3	gnti or gnt adj I	DERWENT	2001/12/18 13:34
3	15	gnti or gnt adj I	USPAT	2001/12/18 13:34

(FILE 'HOME' ENTERED AT 13:14:08 ON 18 DEC 2001)

FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE' ENTERED AT 13:14:18 ON 18 DEC 2001
L1 3260 S ACETYLGLUCOSAMINYLTRANSFERASE?
L2 119 S GNTI OR GTN I
L3 3342 S L1 OR L2
L4 138 S L3 AND (ARABIDOPSIS OR THALIANA OR PLANT OR POTATO OR TOBACC
L5 83 DUP REM L4 (55 DUPLICATES REMOVED)

FILE 'SCISEARCH' ENTERED AT 13:18:37 ON 18 DEC 2001
L6 34 S 91/RVL (S) 1994/RPY (S) GOMEZ ?/RAU

FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE' ENTERED AT 13:23:16 ON 18 DEC 2001
L7 33 S L3 (5A) (ARABIDOPSIS OR THALIANA OR PLANT OR POTATO OR TOBAC
L8 15 DUP REM L7 (18 DUPLICATES REMOVED)

(FILE 'HOME' ENTERED AT 09:27:51 ON 26 JUN 2001)

FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, SCISEARCH' ENTERED AT 09:27:59 ON 26 JUN 2001

L1 3939 S ?ACETYLGLUCOSAMINYLTRANSFERASE? OR GNTI OR GLUCOSAMINYL TRANS
L2 117274 S SOLANUM OR TUBEROSUM OR NICOTIANA OR TABACUM OR ARABIDOPSIS O
L3 45 S L1 AND L2
L4 18 DUP REM L3 (27 DUPLICATES REMOVED)
E VON SCHAEWEN?/AU
E VON SCHAEWEN/AU
L5 2 S E1-E2
L6 63 S E4-E5
L7 65 S L5 OR L6
L8 31 DUP REM L7 (34 DUPLICATES REMOVED)
L9 4 S L8 AND (L1)

L4 ANSWER 1 OF 18 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 2001:300891 CAPLUS
DOCUMENT NUMBER: 134:322353
TITLE: Post-translational modification of recombinant proteins in plants by altering its natural modification abilities
INVENTOR(S): Russell, Douglas; Manjunath, Siva; Bassuner, Ronald
PATENT ASSIGNEE(S): Monsanto Company, USA
SOURCE: PCT Int. Appl., 132 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001029242	A2	20010426	WO 2000-US29027	20001020

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 1999-160758 P 19991021
US 2000-195282 P 20000407

AB The present invention is directed to methods for producing a post-translationally modified heterologous polypeptide in a plant host system by altering the natural post-translational abilities of that plant host system. The post-translational modification may be proteolytic cleavage, glycosylation, phosphorylation,methylation, sulfation, prenylation, acetylation, N-amidation, oxidn., hydroxylation, or myristylation. In a preferred embodiment, this method includes transforming a plant host system with a nucleic acid that encodes a heterologous polypeptide, and isolating that polypeptide from the plant host system. The heterologous proteins may include antibodies and antibody fragments, collagen types I-XX, human protein C, and cytokines. In another aspect of this method, altering the natural post-translational modifications is done by transforming the plant host system with one or more nucleic acid sequences encoding a post-translational modification enzyme. Such plant specific post-translational modifying enzymes include Galactosyl transferase, xylosyl transferase, and fucosyl transferase. In an alternative aspect, the altering is done by mutagenesis of plant host system. In another embodiment, the altering is done by transforming said plant host system with an expression vector comprising a nucleic acid sequence that encodes an antisense nucleic acid. The invention further provides a method for producing a post-translationally modified heterologous polypeptide in a plant host system, by cross-pollinating a first plant, wherein the plant has been transformed with a first expression vector comprising a nucleic acid sequence encoding a heterologous polypeptide, and a second plant wherein the second plant has been transformed with a second expression vector comprising a nucleic acid sequence encoding a post-translational modifying enzyme.

DUPLICATE 1

L4 ANSWER 2 OF 18 MEDLINE
ACCESSION NUMBER: 2000219139 MEDLINE
DOCUMENT NUMBER: 20219139 PubMed ID: 10753899
TITLE: Functional expression of O-linked GlcNAc transferase. Domain structure and substrate specificity.
AUTHOR: Lubas W A; Hanover J A
CORPORATE SOURCE: Laboratory of Cell Biochemistry and Biology, NIDDK, National Institutes of Health, Bethesda, Maryland 20892, USA.
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (2000 Apr 14) 275 (15) 10983-8.
Journal code: HIV; 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200005
ENTRY DATE: Entered STN: 20000518
Last Updated on STN: 20000518
Entered Medline: 20000505

AB O-GlcNAc transferase (OGT) modifies nuclear pore proteins and transcription factors. In **Arabidopsis**, the OGT homolog participates in the gibberellin signaling pathway. We and others have proposed that mammalian OGT is the terminal step in a glucose-sensitive signal transduction pathway that becomes disregulated in insulin resistance. To facilitate mutational analysis of OGT in the absence of competing endogenous activity, we expressed the 103-kDa human OGT in Escherichia coli. Kinetic parameters for the purified recombinant enzyme (K(m) = 1.2 microM for Nup 62; K(m) = 0.5 microM for UDP-GlcNAc) are nearly identical to purified mammalian OGT. Deletions in the highly conserved C terminus result in a complete loss of activity. The N-terminal tetratricopeptide repeat domain is required for optimal recognition of substrates. Removal of the first three tetratricopeptide repeats greatly reduces the O-GlcNAc addition to macromolecular substrates. However, this altered enzyme retains full activity against appropriate synthetic peptides. Autoglycosylation of OGT is augmented when the first six tetratricopeptide repeats are removed showing that these repeats are not required for catalysis. Given its proposed role in modulating insulin action, OGT may modify kinases involved in this signaling cascade. Among the many kinases tested, OGT glycosylates glycogen synthase kinase-3 and casein kinase II, two enzymes critical in the regulation of glycogen synthesis.

DUPLICATE 2

L4 ANSWER 3 OF 18 MEDLINE
ACCESSION NUMBER: 2000498053 MEDLINE
DOCUMENT NUMBER: 20349721 PubMed ID: 10889259
TITLE: Isolation and characterization of plant N-acetyl glucosaminyltransferase I (**GntI**) cDNA sequences. Functional analyses in the **Arabidopsis** cgl mutant and in antisense plants.
AUTHOR: Wenderoth I; von Schaewen A
CORPORATE SOURCE: Pflanzenphysiologie, FB 5 Biologie/Chemie, Universitat Osnabruck, D-49069 Osnabruck, Germany.
SOURCE: PLANT PHYSIOLOGY, (2000 Jul) 123 (3) 1097-108.
Journal code: P98; 0401224. ISSN: 0032-0889.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200010
ENTRY DATE: Entered STN: 20001027
Last Updated on STN: 20001027
Entered Medline: 20001018

AB We report on the isolation and characterization of full-length cDNA

sequences coding for N-**acetylglucosaminyltransferase** I (**GnTI**) from pota[redacted] (**Solanum tuberosum** L.), tobacco (**Nicoti[redacted] tabacum** L.), and **Arabidopsis**. The deduced polypeptide sequences show highest homology among the solanaceous species (93% identity between potato and tobacco compared with about 75% with **Arabidopsis**) but share only weak homology with human **GnTI** (35% identity). In contrast to the corresponding enzymes from animals, all plant **GnTI** sequences identified are characterized by a much shorter hydrophobic membrane anchor and contain one putative N-glycosylation site that is conserved in potato and tobacco, but differs in **Arabidopsis**. Southern-blot analyses revealed that **GntI** behaves as a single-copy gene. Northern-blot analyses showed that **GntI**-mRNA expression is largely constitutive. **Arabidopsis** cgl mutants deficient in **GnTI** activity also possess **GntI** mRNA, indicating that they result from point mutations. **GntI**-expression constructs were tested for the ability to relieve the **GnTI** block in protoplasts of the **Arabidopsis** cgl mutant and used to obtain transgenic potato and tobacco plants that display a substantial reduction of complex glycan patterns. The latter observation indicates that production of heterologous glycoproteins with little or no antigenic glycans can be achieved in whole plants, and not in just **Arabidopsis**, using antisense technology.

L4 ANSWER 4 OF 18 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 2001:8126 CAPLUS
DOCUMENT NUMBER: 134:233435
TITLE: Molecular cloning of cDNA encoding N-**acetylglucosaminyltransferase** II from **Arabidopsis thaliana**
AUTHOR(S): Strasser, R.; Steinkellner, H.; Boren, M.; Altmann, F.; Mach, L.; Glossl, J.; Mucha, J.
CORPORATE SOURCE: Zentrum fur Angewandte Genetik, Universitat fur Bodenkultur Wien, Vienna, 1190, Austria
SOURCE: Glycoconjugate J. (2000), Volume Date 1999, 16(12), 787-791
CODEN: GLJOEW; ISSN: 0282-0080
PUBLISHER: Kluwer Academic Publishers
DOCUMENT TYPE: Journal
LANGUAGE: English
AB N-**acetylglucosaminyltransferase** II (GnTII, E.C. 2.4.1.143) is a Golgi enzyme involved in the biosynthesis of glycoprotein-bound N-linked oligosaccharides, catalyzing an essential step in the conversion of oligomannose-type to complex N-glycans. GnTII activity has been detected in both animals and plants. However, while cDNAs encoding the enzyme have already been cloned from several mammalian sources no GnTII homolog has been cloned from plants so far. Here we report the mol. cloning of an **Arabidopsis thaliana** GnTII cDNA with striking homol. to its animal counterparts. The predicted domain structure of A. **thaliana** GnTII indicates a type II transmembrane protein topol. as it has been established for the mammalian variants of the enzyme. Upon expression of A. **thaliana** GnTII cDNA in the baculovirus/insect cell system, a recombinant protein was produced that exhibited GnTII activity.
REFERENCE COUNT: 17
REFERENCE(S):
(1) Altmann, F; Glycobiology 1993, V3, P619 CAPLUS
(3) Breton, C; Curr Opin Struct Biol 1999, V9, P563 CAPLUS
(4) Breton, C; J Biochem 1998, V123, P1000 CAPLUS
(5) Colley, K; Glycobiology 1997, V7, P1 CAPLUS
(6) D'Agostaro, G; J Biol Chem 1995, V270, P15211 CAPLUS

L4 ANSWER 5 OF 18 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 2000:293467 CAPLUS
DOCUMENT NUMBER: 133:131486
TITLE: Structure of O-Linked GlcNAc Transferase: Mediator of Glycan-Dependent Signaling
AUTHOR(S): Roos, Mark D.; Hanover, John A.
CORPORATE SOURCE: Laboratory of Cell Biochemistry and Biology, NIDDK, National Institutes of Health, Bethesda, MD, 20892, USA
SOURCE: Biochem. Biophys. Res. Commun. (2000), 271(2), 275-280
CODEN: BBRCA9; ISSN: 0006-291X
PUBLISHER: Academic Press
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English
AB A review with 39 refs. The following topics are covered: the tetratricopeptide repeat (TPR); conserved domain I; conserved domain II; **Arabidopsis** spindly locus and gibberellin signaling; deletionsl anal. of OGT; microbial OGT; summary of OGT structure; physiol. role of OGT; the hexosamine biosynthetic pathway. (c) 2000 Academic Press.
REFERENCE COUNT: 39
REFERENCE(S):
(1) Breton, C; Curr Opin Struct Biol 1999, V9, P563 CAPLUS
(2) Chou, T; Proc Natl Acad Sci USA 1995, V92, P4417 CAPLUS
(3) Comer, F; Biochim Biophys Acta 1999, V1473, P161 CAPLUS
(4) Crook, E; Diabetes 1993, V42, P1289 CAPLUS
(5) Das, A; EMBO J 1998, V17, P1192 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 6 OF 18 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 2001:93182 BIOSIS
DOCUMENT NUMBER: PREV200100093182
TITLE: Molecular cloning of N-**acetylglucosaminyltransferase** * II from ***Arabidopsis thaliana**.
AUTHOR(S): Strasser, Richard (1); Steinkellner, Herta (1); Boren, Max (1); Altmann, Friedrich; Mach, Lukas (1); Gloessl, Josef (1); Mucha, Jan (1)
CORPORATE SOURCE: (1) Centre for Applied Genetics, University of Agricultural Sciences, Vienna Austria
SOURCE: Glycoconjugate Journal, (January February, 2000) Vol. 17, No. 1-2, pp. 78. print.
Meeting Info.: Second International Glycosyltransferase Symposium Toronto, Ontario, Canada May 12-14, 2000
ISSN: 0282-0080.
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English

L4 ANSWER 7 OF 18 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 2001:93180 BIOSIS
DOCUMENT NUMBER: PREV200100093180
TITLE: Isolation and characterization of different plant N-**acetylglucosaminyltransferase** I (**GnTI**) cDNA sequences, and generation of potato and tobacco antisense plants.
AUTHOR(S): Wenderoth, Irina (1); von Schaewen, Antje (1)
CORPORATE SOURCE: (1) Plant Physiology, FB 5, Universitaet Osnabrueck, 49069, Osnabrueck: i.wenderoth@mpb-cologne.com Germany
SOURCE: Glycoconjugate Journal, (January February, 2000) Vol. 17,

No. 1-2, pp. 77. print.
Meeting Info.: Second International Glycosyltransferase Symposium Toronto, Ontario, Canada May 12-14, 2000
ISSN: 0282-0080.
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English

L4 ANSWER 8 OF 18 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1999:384106 CAPLUS
DOCUMENT NUMBER: 131:28652
TITLE: Plant **GntI** sequences, transgenic plants with altered N-acetylglucosamine transferase activity and their use in production of glycoproteins
INVENTOR(S): Von Schaewen, Antje
PATENT ASSIGNEE(S): Germany
SOURCE: Ger. Offen., 36 pp.
CODEN: GWXXBX
DOCUMENT TYPE: Patent
LANGUAGE: German
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
DE 19754622	A1	19990610	DE 1997-19754622	19971209
WO 9929879	A1	19990617	WO 1998-EP8001	19981209
W: AU, CA, JP, US				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
AU 9922688	A1	19990628	AU 1999-22688	19981209
EP 1038014	A1	20000927	EP 1998-966266	19981209
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				

PRIORITY APPLN. INFO.: DE 1997-19754622 A 19971209
WO 1998-EP8001 W 19981209

AB The cDNAs for tobacco, potato and **Arabidopsis thaliana** N-acetylglucosamine transferases (**GntI**'s) as well as the encoded protein sequences are disclosed. Use of **GntI** nucleic acids to create transgenic plants with reduced or nonexistent N-acetylglucosamine transferase activities are also disclosed. These transgenic plants may be used to prep. clin. useful glycoproteins lacking immunogenic plant-specific carbohydrates.

REFERENCE COUNT: 3
REFERENCE(S): (1) Anon; CAPLUS
(2) Anon; CAPLUS
(3) Anon; WO 9621038 CAPLUS

DUPLICATE 3

L4 ANSWER 9 OF 18 MEDLINE
ACCESSION NUMBER: 1999373163 MEDLINE
DOCUMENT NUMBER: 99373163 PubMed ID: 10441510
TITLE: An **Arabidopsis thaliana** cDNA complements the N-**acetylglucosaminyltransferase** I deficiency of CHO Lec1 cells.
AUTHOR: Bakker H; Lommen A; Jordi W; Stiekema W; Bosch D
CORPORATE SOURCE: Department of Molecular Biology, Centre for Plant Breeding and Reproduction Research (CPRO-DLO), Wageningen, 6700AA, The Netherlands.. h.bakker@cpro.dlo.nl
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (1999 Aug 11) 261 (3) 829-32.
Journal code: 9Y8; 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English

FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AJ243198
ENTRY MONTH: 9909
ENTRY DATE: Entered STN: 19990925
Last Updated on STN: 19990925
Entered Medline: 19990909

AB N-**Acetylglucosaminyltransferase** I (GlcNAcT-I, EC 2.4.1.101) is the enzyme which initiates the formation of complex N-linked glycans in eukaryotes by transforming GlcNAc to the oligo-mannosyl acceptor Man(5)GlcNAc(2)-Asn. The enzymatic activity and the structure that is synthesised by this enzyme are found in animals and plants but not in yeast. cDNAs encoding the enzyme have already been cloned from several mammals and the nematode Caenorhabditis elegans. In this article the cloning of an **Arabidopsis thaliana** GlcNAcT-I cDNA with homology to animal cDNAs is described. By expression of the plant cDNA in CHO Lec1 cells, a mammalian cell line deficient in GlcNAcT-I, it was shown that it encodes an active enzyme with the same enzymatic activity as the animal homologue. It has already been shown that a human GlcNAcT-I can complement an A. **thaliana** mutant (cgl-1). Here it is shown that the reverse is also true, the plant glycosyltransferase is able to complement a mammalian mutant (Lec1) deficient in GlcNAcT-I.

DUPLICATE 4

L4 ANSWER 10 OF 18 MEDLINE
ACCESSION NUMBER: 2001145267 MEDLINE
DOCUMENT NUMBER: 21019070 PubMed ID: 11229321
TITLE: Molecular cloning of cDNA encoding N-**acetylglucosaminyltransferase** II from **Arabidopsis thaliana**.
AUTHOR: Strasser R; Steinkellner H; Boren M; Altmann F; Mach L; Glossl J; Mucha J
CORPORATE SOURCE: Zentrum fur Angewandte Genetik, Universitat fur Bodenkultur Wien, Austria.
SOURCE: GLYCOCONJUGATE JOURNAL, (1999 Dec) 16 (12) 787-91. Journal code: BJJ; 8603310. ISSN: 0282-0080.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-UNKNOWN
ENTRY MONTH: 200103
ENTRY DATE: Entered STN: 20010404
Last Updated on STN: 20010404
Entered PubMed: 20001229
Entered Medline: 20010315

AB N-**acetylglucosaminyltransferase** II (GnTII, EC 2.4.1.143) is a Golgi enzyme involved in the biosynthesis of glycoprotein-bound N-linked oligosaccharides, catalysing an essential step in the conversion of oligomannose-type to complex N-glycans. GnTII activity has been detected in both animals and plants. However, while cDNAs encoding the enzyme have already been cloned from several mammalian sources no GnTII homologue has been cloned from plants so far. Here we report the molecular cloning of an **Arabidopsis thaliana** GnTII cDNA with striking homology to its animal counterparts. The predicted domain structure of A. **thaliana** GnTII indicates a type II transmembrane protein topology as it has been established for the mammalian variants of the enzyme. Upon expression of A. **thaliana** GnTII cDNA in the baculovirus/insect cell system, a recombinant protein was produced that exhibited GnTII activity.

DUPLICATE 5

L4 ANSWER 11 OF 18 MEDLINE
ACCESSION NUMBER: 1999335389 MEDLINE

DOCUMENT NUMBER: 99335389 PubMed ID: 10406843
TITLE: Molecular cloning and characterization of cDNA coding for beta1, 2N-**acetylglucosaminyltransferase** I (GlcNAc-TI) from **Nicotiana tabacum**.
AUTHOR: Strasser R; Mucha J; Schwihla H; Altmann F; Glossl J; Steinkellner H
CORPORATE SOURCE: Zentrum fur Angewandte Genetik and 1Institut fur Chemie, Universitat fur Bodenkultur Wien, Muthgasse 18, A-1190 Vienna, Austria.
SOURCE: GLYCOBIOLOGY, (1999 Aug) 9 (8) 779-85.
Journal code: BEL; 9104124. ISSN: 0959-6658.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-Y16832
ENTRY MONTH: 199910
ENTRY DATE: Entered STN: 19991026
Last Updated on STN: 19991026
Entered Medline: 19991014

AB In plants as well as in animals beta1, 2N-**acetylglucosaminyltransfera se** I (GlcNAc-TI) is a Golgi resident enzyme that catalyzes an essential step in the biosynthetic pathway leading from oligomannosidic N-glycans to complex or hybrid type N-linked oligosaccharides. Employing degenerated primers deduced from known GlcNAc-TI genes from animals, we were able to identify the cDNA coding for GlcNAc-TI from a **Nicotiana tabacum** cDNA library. The complete nucleotide sequence revealed a 1338 base pair open reading frame that codes for a polypeptide of 446 amino acids. Comparison of the deduced amino acid sequence with that of already known GlcNAc-TI polypeptides revealed no similarity of the tobacco clone within the putative cytoplasmatic, transmembrane, and stem regions. However, 40% sequence similarity was found within the putative C-terminal catalytic domain containing conserved single amino acids and peptide motifs. The predicted domain structure of the tobacco polypeptide is typical for type II transmembrane proteins and comparable to known GlcNAc-TI from animal species. In order to confirm enzyme activity a truncated form of the protein containing the putative catalytic domain was expressed using a baculovirus/insect cell system. Using pyridylaminated Man(5)- or Man(3)GlcNAc(2)as acceptor substrates and HPLC analysis of the products GlcNAc-TI activity was shown. This demonstrates that the C-terminal region of the protein comprises the catalytic domain. Expression of GlcNAc-TI mRNA in tobacco leaves was detected using RT-PCR. Southern blot analysis gave two hybridization signals of the gene in the amphidiploid genomes of the two investigated species N. **tabacum** and N.benthamiana.

L4 ANSWER 12 OF 18 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 2000:264086 CAPLUS
DOCUMENT NUMBER: 133:220187
TITLE: Genetic and biochemical analysis of **arabidopsis** SPY
AUTHOR(S): Thornton, T.; Kreppel, L.; Hart, G.; Olszewski, N.
CORPORATE SOURCE: Department of Plant Biology, University of Minnesota, USA
SOURCE: Curr. Plant Sci. Biotechnol. Agric. (1999), 36(Plant Biotechnology and In Vitro Biology in the 21st Century), 445-448
CODEN: CPBAE2; ISSN: 0924-1949
PUBLISHER: Kluwer Academic Publishers
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The **arabidopsis** SPY protein is a neg. regulator of gibberellin signal transduction and, based on protein sequence similarity, is

hypothesized to be a O-GlcNAc transferase (OGT). Proteins from spy mutants were found to exhibit allele-specific alterations in the pattern of GlcNAc modification. Insect cell-expressed SPY is GlcNAc-modified and preliminary activity assays indicated that this protein has OGT activity.

REFERENCE COUNT: 13
REFERENCE(S):
(1) Haltiwanger, R; J Biol Chem 1990, V265, P2563 CAPLUS
(2) Haltiwanger, R; J Biol Chem 1992, V267, P9005 CAPLUS
(3) Heese-Peck, A; Plant Cell 1995, V7, P1459 CAPLUS
(4) Heese-Peck, A; Plant Cell 1998, V10, P599 CAPLUS
(5) Jacobsen, S; Plant Cell 1993, V5, P887 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 13 OF 18 SCISEARCH COPYRIGHT 2001 ISI (R)
ACCESSION NUMBER: 1999:797504 SCISEARCH
THE GENUINE ARTICLE: 245XW
TITLE: Overexpression of a gene that encodes the first enzyme in the biosynthesis of asparagine-linked glycans makes plants resistant to tunicamycin and obviates the tunicamycin-induced unfolded protein response
AUTHOR: Koizumi N; Ujino T; Sano H; Chrispeels M J (Reprint)
CORPORATE SOURCE: NARA INST SCI & TECHNOL, 8916-5 TAKAYAMA, NARA 6300101, JAPAN (Reprint); NARA INST SCI & TECHNOL, NARA 6300101, JAPAN; UNIV CALIF SAN DIEGO, DEPT BIOL, LA JOLLA, CA 92093
COUNTRY OF AUTHOR: JAPAN; USA
SOURCE: PLANT PHYSIOLOGY, (OCT 1999) Vol. 121, No. 2, pp. 353-361.
Publisher: AMER SOC PLANT PHYSIOLOGISTS, 15501 MONONA DRIVE, ROCKVILLE, MD 20855.
ISSN: 0032-0889.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE; AGRI
LANGUAGE: English
REFERENCE COUNT: 49
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB The cytotoxic drug tunicamycin kills cells because it is a specific inhibitor of UDP-N-acetylglucosamine:dolichol phosphate N-acetylglucosamine-1-P transferase (GPT), an enzyme that catalyzes the initial step of the biosynthesis of dolichol-linked oligosaccharides. In the presence of tunicamycin, asparagine-linked glycoproteins made in the endoplasmic reticulum are not glycosylated with N-linked glycans, and therefore may not fold correctly. Such proteins may be targeted for breakdown. Cells that are treated with tunicamycin normally experience an unfolded protein response and induce genes that encode endoplasmic reticulum chaperones such as the binding protein (BiP). We isolated a cDNA clone for **Arabidopsis** GPT and overexpressed it in **Arabidopsis**. The transgenic plants have a 10-fold higher level of GPT activity and are resistant to 1 mu g/mL tunicamycin, a concentration that kills control plants. Transgenic plants grown in the presence of tunicamycin have N-glycosylated proteins and the drug does not induce BiP mRNA levels as it does in control plants. BiP mRNA levels are highly induced in both control and CPT-expressing plants by azetidine-2-carboxylate. These observations suggest that excess GPT activity obviates the normal unfolded protein response that cells experience when exposed to tunicamycin.

DUPLICATE 6

L4 ANSWER 14 OF 18 MEDLINE
ACCESSION NUMBER: 1999330190 MEDLINE
DOCUMENT NUMBER: 99330190 PubMed ID: 10403396
TITLE: The N-terminal 77 amino acids from tobacco N-

acetylglucosaminyltransferase I are sufficient to retain a reporter protein in the Golgi apparatus of **Nicotiana** benthamiana cells.

AUTHOR: Essl D; Dirnberger D; Gomord V; Strasser R; Faye L; Glossl J; Steinkellner H

CORPORATE SOURCE: Zentrum fur Angewandte Genetik, Universitat fur Bodenkultur-Wien, Austria.

SOURCE: FEBS LETTERS, (1999 Jun 18) 453 (1-2) 169-73.
Journal code: EUH; 0155157. ISSN: 0014-5793.

PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199908

ENTRY DATE: Entered STN: 19990816
Last Updated on STN: 19990816
Entered Medline: 19990802

AB In order to investigate sequences of tobacco N-**acetylglucosaminyltransferase** I (**GnTI**), involved in targeting to and retention in the plant Golgi apparatus the cytoplasmic transmembrane stem (CTS) region of the enzyme was cloned in frame with the cDNA of the green fluorescent protein (gfp) and subsequently transiently expressed in **Nicotiana** benthamiana plants using a tobacco mosaic virus (TMV) based expression vector. Confocal laser scanning microscopy showed small fluorescent vesicular bodies in CTS-gfp expressing cells, while gfp alone expressed in control plants was uniformly distributed in the cytoplasm. The CTS-gfp fusion protein colocalised with immunolabelling observed by an antibody specific for the Golgi located plant Lewis a epitope. Furthermore, treatment with brefeldin A, a Golgi specific drug, resulted in the formation of large fluorescent vesiculated areas. These results strongly suggest a Golgi location for CTS-gfp and as a consequence our findings reveal that the N-terminal 77 amino acids of tobacco **GnTI** are sufficient to target to and to retain a reporter protein in the plant Golgi apparatus and that TMV based vectors are suitable vehicles for rapid delivery of recombinant proteins to the secretory pathway.

L4 ANSWER 15 OF 18 MEDLINE DUPLICATE 7

ACCESSION NUMBER: 94173922 MEDLINE

DOCUMENT NUMBER: 94173922 PubMed ID: 8127889

TITLE: Complementation of an **Arabidopsis thaliana** mutant that lacks complex asparagine-linked glycans with the human cDNA encoding N-**acetylglucosaminyltransferase** I.

AUTHOR: Gomez L; Chrispeels M J

CORPORATE SOURCE: Department of Biology, University of California at San Diego, La Jolla 92093-0116.

SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1994 Mar 1) 91 (5) 1829-33.
Journal code: PV3; 7505876. ISSN: 0027-8424.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199404

ENTRY DATE: Entered STN: 19940420
Last Updated on STN: 19940420
Entered Medline: 19940411

AB N-**Acetylglucosaminyltransferase** I (EC 2.4.1.101) initiates the conversion of high-mannose asparagine-linked glycans to complex asparagine-linked glycans in plant as well as in animal cells. This Golgi enzyme is missing in the cgl mutant of **Arabidopsis**

thaliana, and the mutant cells are unable to synthesize complex glycans. Transformation of cells from the mutant plants with the cDNA encoding human **acetylglucosaminyltransferase** I restores the wild-type phenotype of the plant cells. Fractionation of the subcellular organelles on isopycnic sucrose gradients shows that the human enzyme in the complemented cells bands at the same density, 1.14 g/cm3, typical of Golgi cisternae, as the enzyme in the wild-type plant cells. These results demonstrate that complementation results from the presence of the human enzyme in the plant Golgi apparatus, where it is functionally integrated into the biosynthetic machinery of the plant cell. In addition, given the evolutionary distance between plants and mammals and the great diversity of glycoproteins that are modified in each, there is probably no specific recognition between this Golgi enzyme and the polypeptide domains of the proteins it modifies.

L4 ANSWER 16 OF 18 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 1994:311953 BIOSIS
DOCUMENT NUMBER: PREV199497324953
TITLE: Distribution of xylosylation and fucosylation in the plant Golgi apparatus.
AUTHOR(S): Fitchette-Laine, Anne-Catherine; Gomord, Veronique; Chekkafi, Aicha; Faye, Loic (1)
CORPORATE SOURCE: (1) LTI-CNRS URA 203, European Inst. Peptide Res., Univ. Rouen, 76821 Mont-Saint-Aignan Cedex France
SOURCE: Plant Journal, (1994) Vol. 5, No. 5, pp. 673-682. ISSN: 0960-7412.
DOCUMENT TYPE: Article
LANGUAGE: English

AB Antibodies have been immunopurified which are specific for carbohydrate epitopes containing the beta-1 fwdarw 2 xylose or alpha-1 fwdarw 3 fucose residues found on complex N-linked glycans in plants. The antibody specificity was determined by taking advantage of an **Arabidopsis thaliana** N-glycosylation mutant which lacks N-acetyl-glucosaminyltransferase I and is unable to synthesize complex glycans. These antibodies were used to immunolocalize xylose- and fucose-containing glycoproteins in suspension-cultured sycamore cells (Acer pseudoplatanus). By mapping the enzymatic reaction products within the Golgi apparatus, the fucosyl- and xylosyltransferase subcellular localization was made possible using immunocytochemistry on thin sections of high-pressure frozen and freeze-substituted sycamore cells. This procedure allows a much better preservation of organelles, and particularly of the Golgi stack morphology, than that obtained with conventionally fixed samples. Glycoproteins containing beta-1 fwdarw 2 xylose and alpha-1 fwdarw 3 fucose residues were immunodetected in the cell wall, the vacuole, and the Golgi cisternae. The extent of immunolabeling over the different cisternae of 50 Golgi stacks was quantified after treatment with antixylose or anti-fucose antibodies. Labeling for xylose-containing glycoproteins was predominant in the medial cisternae, while fucose-containing glycoproteins were mainly detected in the trans compartment. Therefore, in plants, complex N-linked glycan xylosylation probably occurs mostly at the medial Golgi level and alpha-1 fwdarw 3 fucose is mainly incorporated in the trans cisternae. Finally, fucose- and xylose-containing glycoproteins were also immunolocalized, albeit to a lesser extent, in earlier Golgi compartments. This indicates that the glycosylation events are a continuous process with some maxima in given compartments, rather than a succession of discrete and compartment-dependent steps.

L4 ANSWER 17 OF 18 MEDLINE DUPLICATE 8
ACCESSION NUMBER: 94105339 MEDLINE
DOCUMENT NUMBER: 94105339 PubMed ID: 8278542
TITLE: Isolation of a mutant **Arabidopsis** plant that lacks N-acetyl **glucosaminyl transferase** I and is unable to synthesize Golgi-modified complex N-linked glycans.
AUTHOR: **von Schaewen A; Sturm A; O'Neill J; Chrispeels M J**
CORPORATE SOURCE: Department of Biology, University of California, San Diego,
La Jolla 92093-0116.
SOURCE: PLANT PHYSIOLOGY, (1993 Aug) 102 (4) 1109-18.
Journal code: P98; 0401224. ISSN: 0032-0889.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199402
ENTRY DATE: Entered STN: 19940218
Last Updated on STN: 19940218
Entered Medline: 19940210

AB The complex asparagine-linked glycans of plant glycoproteins, characterized by the presence of beta 1-->2 xylose and alpha 1-->3 fucose residues, are derived from typical mannose9(N-acetylglucosamine)2 (Man9GlcNAc2) N-linked glycans through the activity of a series of glycosidases and glycosyl transferases in the Golgi apparatus. By screening leaf extracts with an antiserum against complex glycans, we isolated a mutant of **Arabidopsis thaliana** that is blocked in the conversion of high-manne to complex glycans. In callus tissues derived from the mutant plants, all glycans bind to concanavalin A. These glycans can be released by treatment with endoglycosidase H, and the majority has the same size as Man5GlcNAc1 glycans. In the presence of deoxymannojirimycin, an inhibitor of mannosidase I, the mutant cells synthesize Man9GlcNAc2 and Man8GlcNAc2 glycans, suggesting that the biochemical lesion in the mutant is not in the biosynthesis of high-mannose glycans in the endoplasmic reticulum but in their modification in the Golgi. Direct enzyme assays of cell extracts show that the mutant cells lack N-acetyl **glucosaminyl transferase** I, the first enzyme in the pathway of complex glycan biosynthesis. The mutant plants are able to complete their development normally under several environmental conditions, suggesting that complex glycans are not essential for normal developmental processes. By crossing the complex-glycan-deficient strain of A. **thaliana** with a transgenic strain that expresses the glycoprotein phytohemagglutinin, we obtained a unique strain that synthesizes phytohemagglutinin with two high-mannose glycans, instead of one high-mannose and one complex glycan.

L4 ANSWER 18 OF 18 SCISEARCH COPYRIGHT 2001 ISI (R)
ACCESSION NUMBER: 91:390095 SCISEARCH
THE GENUINE ARTICLE: FV925
TITLE: PROMOTERS OF AUXIN-INDUCED GENES FROM TOBACCO CAN LEAD TO AUXIN-INDUCIBLE AND ROOT TIP-SPECIFIC EXPRESSION
AUTHOR: VANDERZAAL E J (Reprint); DROOG F N J; BOOT C J M; HENSGENS L A M; HOGE J H C; SCHILPEROORT R A; LIBBENGA K R
CORPORATE SOURCE: LEIDEN UNIV, DEPT PLANT MOLEC BIOL, CLUSIUS LAB, WASSENAARSEWEG 64, 2333 AL LEIDEN, NETHERLANDS (Reprint); BOT LAB, 2311 VJ LEIDEN, NETHERLANDS
COUNTRY OF AUTHOR: NETHERLANDS
SOURCE: PLANT MOLECULAR BIOLOGY, (1991) Vol. 16, No. 6, pp. 983-998.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE; AGRI

L4 ANSWER 17 OF 18 MEDLINE DUPLICATE 8
ACCESSION NUMBER: 94105339 MEDLINE
DOCUMENT NUMBER: 94105339 PubMed ID: 8278542
TITLE: Isolation of a mutant **Arabidopsis** plant that lacks N-acetyl **glucosaminyl transferase** I and is unable to synthesize Golgi-modified complex N-linked glycans.
AUTHOR: von Schaewen A; Sturm A; O'Neill J; Chrispeels M J
CORPORATE SOURCE: Department of Biology, University of California, San Diego, La Jolla 92093-0116.
SOURCE: PLANT PHYSIOLOGY, (1993 Aug) 102 (4) 1109-18. Journal code: P98; 0401224. ISSN: 0032-0889.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199402
ENTRY DATE: Entered STN: 19940218
Last Updated on STN: 19940218
Entered Medline: 19940210

AB The complex asparagine-linked glycans of plant glycoproteins, characterized by the presence of beta 1-->2 xylose and alpha 1-->3 fucose residues, are derived from typical mannose9(N-acetylglucosamine)2 (Man9GlcNAc2) N-linked glycans through the activity of a series of glycosidases and glycosyl transferases in the Golgi apparatus. By screening leaf extracts with an antiserum against complex glycans, we isolated a mutant of **Arabidopsis thaliana** that is blocked in the conversion of high-manne to complex glycans. In callus tissues derived from the mutant plants, all glycans bind to concanavalin A. These glycans can be released by treatment with endoglycosidase H, and the majority has the same size as Man5GlcNAc1 glycans. In the presence of deoxymannojirimycin, an inhibitor of mannosidase I, the mutant cells synthesize Man9GlcNAc2 and Man8GlcNAc2 glycans, suggesting that the biochemical lesion in the mutant is not in the biosynthesis of high-mannose glycans in the endoplasmic reticulum but in their modification in the Golgi. Direct enzyme assays of cell extracts show that the mutant cells lack N-acetyl **glucosaminyl transferase** I, the first enzyme in the pathway of complex glycan biosynthesis. The mutant plants are able to complete their development normally under several environmental conditions, suggesting that complex glycans are not essential for normal developmental processes. By crossing the complex-glycan-deficient strain of A. **thaliana** with a transgenic strain that expresses the glycoprotein phytohemagglutinin, we obtained a unique strain that synthesizes phytohemagglutinin with two high-mannose glycans, instead of one high-mannose and one complex glycan.

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ACCESSION NUMBER: 91:390095 SCISEARCH
THE GENUINE ARTICLE: FV925
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AUTHOR: VANDERZAAL E J (Reprint); DROOG F N J; BOOT C J M; HENSGENS L A M; HOGE J H C; SCHILPEROORT R A; LIBBENGA K R
CORPORATE SOURCE: LEIDEN UNIV, DEPT PLANT MOLEC BIOL, CLUSIUS LAB, WASSENAARSEWEG 64, 2333 AL LEIDEN, NETHERLANDS (Reprint); BOT LAB, 2311 VJ LEIDEN, NETHERLANDS
COUNTRY OF AUTHOR: NETHERLANDS
SOURCE: PLANT MOLECULAR BIOLOGY, (1991) Vol. 16, No. 6, pp. 983-998.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE; AGRI

LANGUAGE: ENGLISH
REFERENCE COUNT: [redacted]

[redacted]STRACT IS AVAILABLE IN THE ALL [redacted]D IALL FORMATS*

AB In previous studies we have identified several mRNAs which accumulate after addition of 2,4-dichloro-phenoxyacetic-acid (2,4-D) to auxin-starved tobacco cells [45, 46]. The mRNAs corresponding to cDNA clone pCNT103 were found to accumulate transiently prior to the cell division response due to auxin treatment. In this study we determined the sequences of three 103-like cDNAs and two 103-like genes, **GNT1** and GNT35. To further study the regulation of the expression of these genes their 5' regions were translationally fused with the beta-D-glucuronidase reporter gene (GUS). The **GNT1** 5' region led to GUS expression only in the root tips of transgenic plants. By using transgenic hairy-root cultures and transformed cell suspension cultures it was shown that the 5' regions of both **GNT1** and GNT35 lead to 2,4-D-inducible expression of GUS activity. The homology of the 103-like genes with other auxin-regulated genes is evaluated.